

Kew

Royal Botanic Gardens

Applying personalized genomics to ash trees

Professor Richard Buggs

@RJABuggs

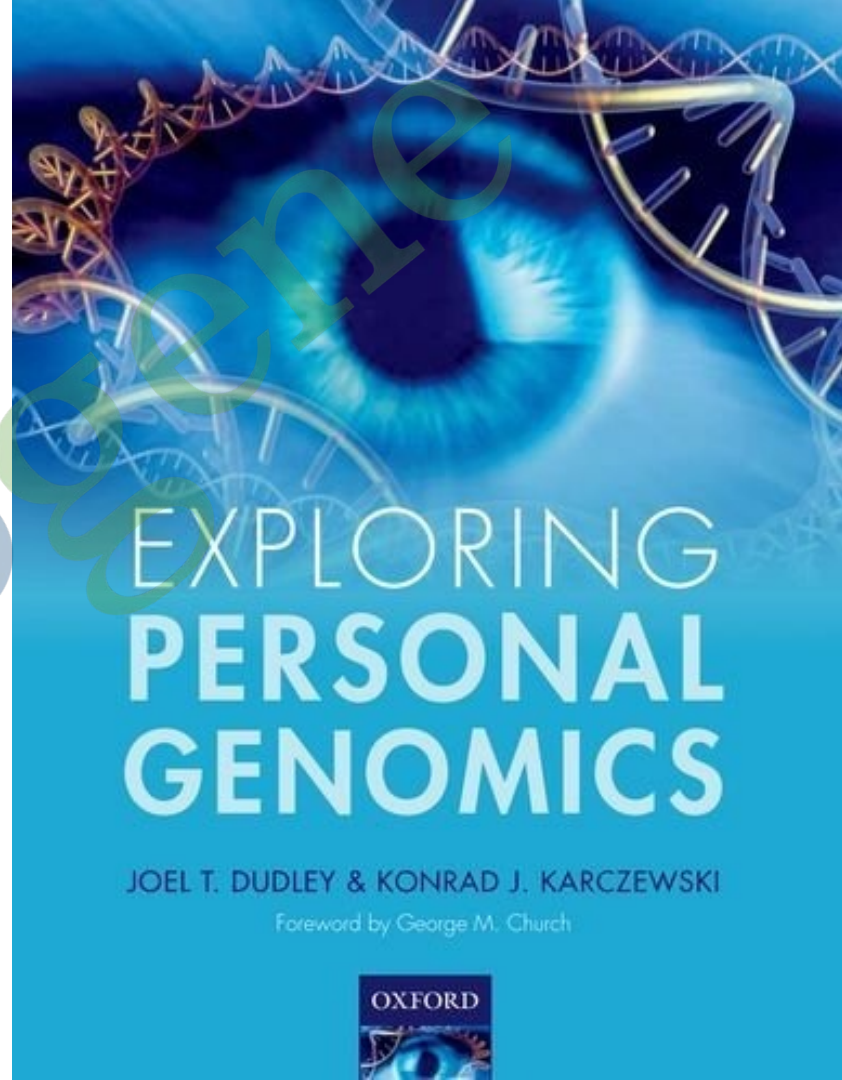


Queen Mary
University of London



Queen Mary
University of London

2012





Broad-leaved trees are experimentally intractable but genomically tractable

	Wheat	Ash
Generation time	< 1 year	> 10 years
Time to harvest	< 1 year	> 30 years
Space to grow	0.1 x 0.1 x 1 m	5 x 5 x 30 m
Inbred lines	Available	Unavailable
Genome size	17 Gbp	0.9 Gbp

GB trees: woodland areas and genome sizes

Species	Hectares	Genome size (~)
Sitka spruce	692,000	20 Gbp
Scots pine	227,000	22 Gbp
Oak	223,000	0.9 Gbp
Birch	160,000	0.5 Gbp
Lodgepole pine	135,000	19 Gbp
Ash	129,000	0.9 Gbp
Japanese/hybrid larch	111,000	13 Gbp

The world needs trees

Royal Botanic Gardens
Kew

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Climate change: Trees 'most effective solution' for warming

By Matt McGrath
Environment correspondent

🕒 4 July 2019

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Increasing biotic threats to trees

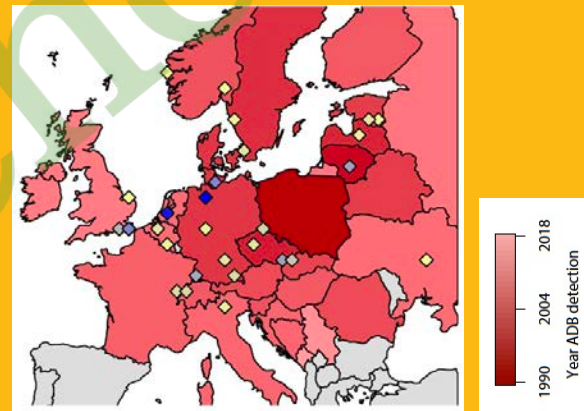
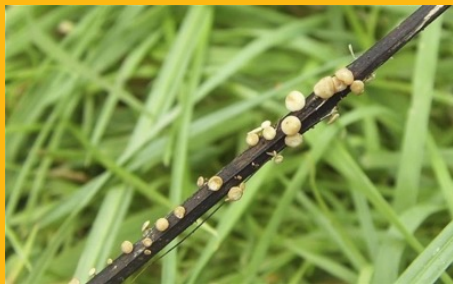


www.shipmap.org/

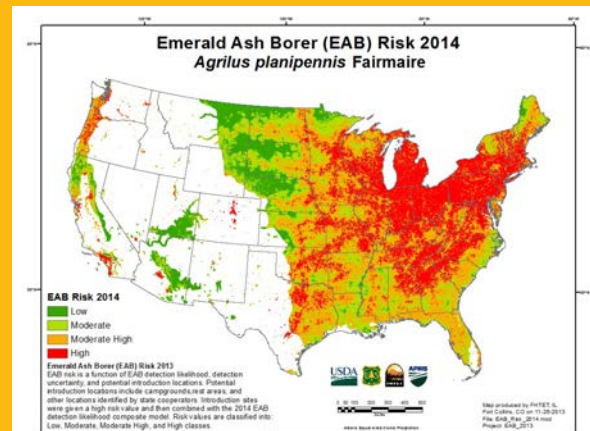


Alien invasive threats to ash trees

Ash Dieback (*Hymenoscyphus fraxineus*)



Emerald Ash Borer (*Agrilus planipennis*)

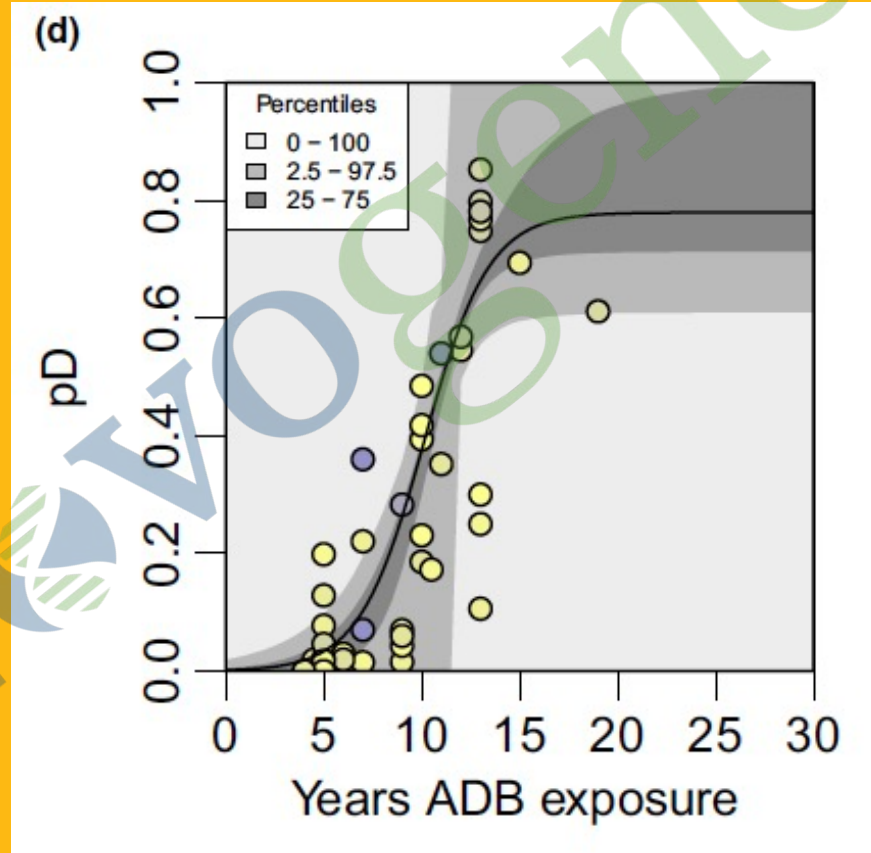


Estimating mortality rates of European ash

A three-parameter logistic model for ash mortality due to ash dieback based on data sets from sites across Europe



Dr Tim Coker



White ash (USA)



© The Morton Arboretum

Fraxinus americana

<http://dx.doi.org/10.2305/IUCN.UK.2017-2.RLTS.T61918430A61918432.en>

Scope: Global
Language: English

[Download assessment](#)

NOT EVALUATED	DATA DEFICIENT	LEAST CONCERN	NEAR THREATENED	VULNERABLE	ENDANGERED	CRITICALLY ENDANGERED	EXTINCT IN THE WILD	EXTINCT
NE	DD	LC	NT	VU	EN	CR	EW	EX

Summary

[Classification Schemes](#)

[Images & External Links](#)

[Bibliography](#)

[Full Account](#)

Taxonomy [\[top\]](#)

Kingdom	Phylum	Class	Order	Family
Plantae	Tracheophyta	Magnoliopsida	Scrophulariales	Oleaceae

Scientific Name: *Fraxinus americana* L.

Common Name(s):
English – White Ash

[Taxonomy](#)
[Assessment Information](#)
[Geographic Range](#)
[Population](#)
[Habitat and Ecology](#)
[Use and Trade](#)
[Threats](#)
[Conservation Actions](#)

Translate page into:

VIEW MAP

Genome sequence and genetic diversity of European ash trees

Elizabeth S. A. Sollars^{1,2*}, Andrea L. Harper^{3*}, Laura J. Kelly^{1*}, Christine M. Sambles^{4*}, Ricardo H. Ramirez-Gonzalez⁵, David Swarbreck⁵, Gemy Kaithakottil⁵, Endymion D. Cooper¹, Cristobal Uauy⁶, Lenka Havlickova³, Gemma Worswick^{1,8}, David J. Studholme⁴, Jasmin Zohren¹, Deborah L. Salmon⁴, Bernardo J. Clavijo⁵, Yi Li³, Zhesi He³, Alison Fellgett³, Lea Vig McKinney⁷, Lene Rostgaard Nielsen⁷, Gerry C. Douglas⁸, Erik Dahl Kjær⁷, J. Allan Downie⁶, David Boshier⁹, Steve Lee¹⁰, Jo Clark¹¹, Murray Grant^{4†}, Ian Bancroft³, Mario Caccamo^{5,12} & Richard J. A. Buggs^{1,13}

1. Queen Mary University of London. **2.** QIAGEN Aarhus, Denmark. **3.** The Earlham Institute, Norwich. **4.** University of Oxford. **5.** The Earth Trust, Abingdon. **6.** Forest Research, Northern Research Station, Roslin. **7.** University of York. **8.** University of Exeter. **9.** University of Copenhagen, Denmark. **10.** Teagasc, Ireland. **11.** John Innes Centre, Norwich **12.** Royal Botanical Gardens, Kew

Lizzy
Sollars



Dr Laura
Kelly



Jasmin
Zohren



Dr Endymion
Cooper



Ash Tree Genomes



Queen Mary
University of London

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WELCOME TO ASH TREE GENOMES



This website hosts ash genome data to assist scientists in the search for genes that may confer resistance to ash dieback (*Hymenoscyphus fraxinea*) and the emerald ash borer (*Agrilus planipennis*).

Scientists at Queen Mary, University of London (QMUL) in Richard Buggs' lab have sequenced the genome of the European ash tree (*Fraxinus excelsior*), funded by an urgency grant awarded by the Natural Environment Research Council in 2013. The ash genome and associated data have now been published in *Nature*. The paper is available open access [here](#).

The tree sequenced was the result of self-pollination of a tree growing in woodland in Oxfordshire. The controlled self-pollination of the parent tree was carried out by Dr David Boshier of Oxford University. The offspring from this self-pollination are growing at Paradise Wood in Oxfordshire, owned by the Earth Trust, and managed by Jo

Genomic basis of European ash tree resistance to ash dieback fungus

Jonathan J. Stocks^{1,2}, Carey L. Metherringham^{1,2}, William J. Plumb^{1,2,3}, Steve J. Lee⁴, Laura J. Kelly^{1,2}, Richard A. Nichols¹ and Richard J. A. Buggs^{1,2*}

Jonathan
Stocks



Carey
Metherringham



Will Plumb

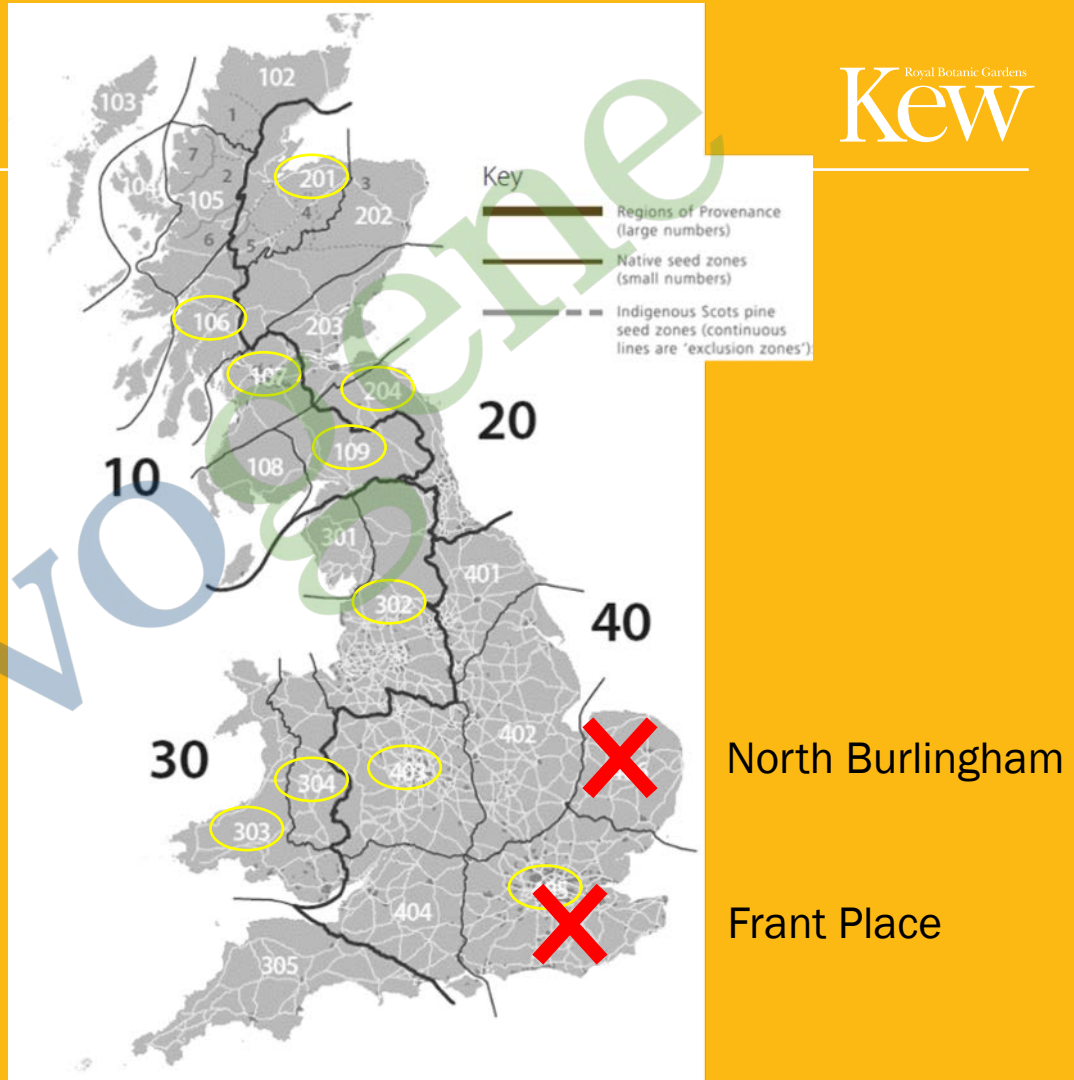


Dr Laura
Kelly



Forest Research mass screening trials

- Set up in 2012/13
- 14 sites
- 15 provenances
- 153,408 trees





**A Forest Research Mass Screening
trial for ash dieback**

missing

1

2

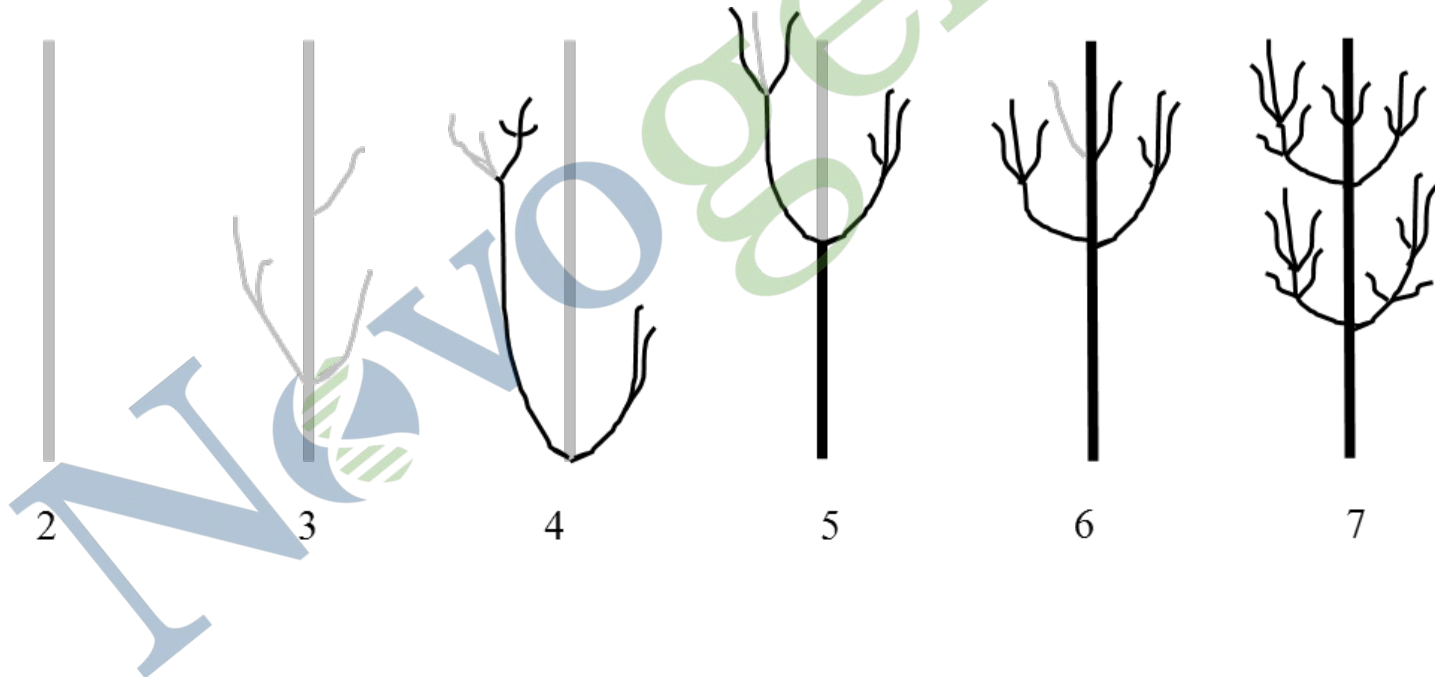
3

4

5

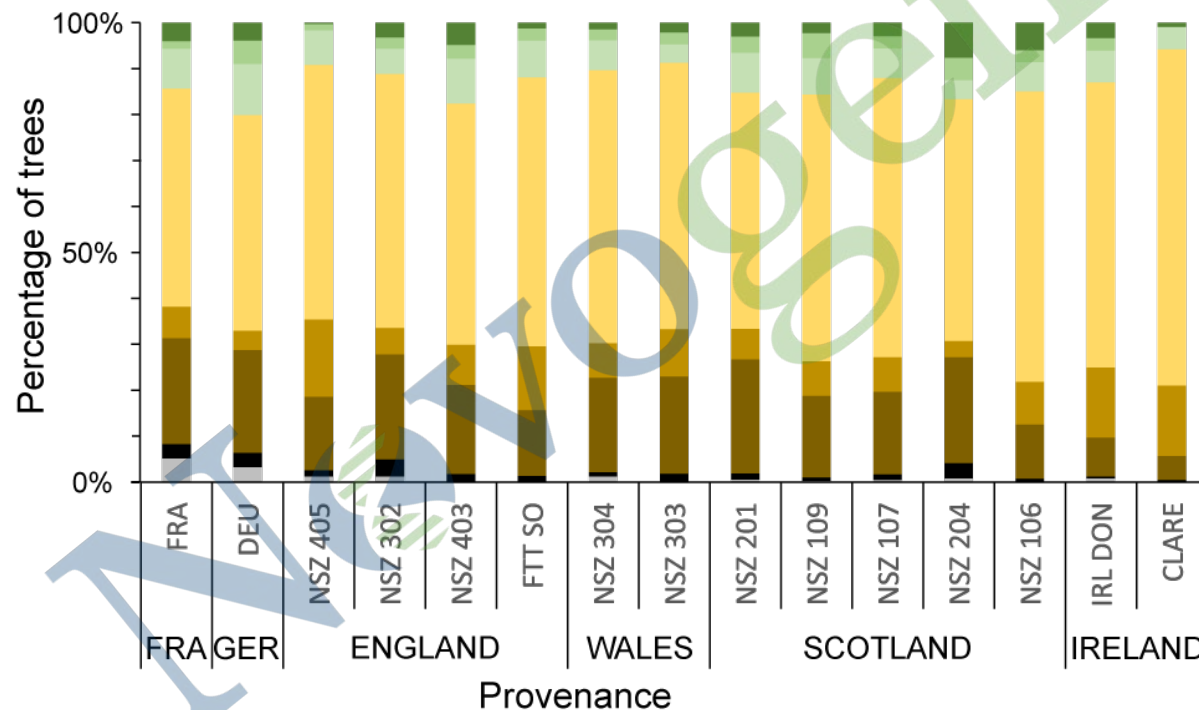
6

7



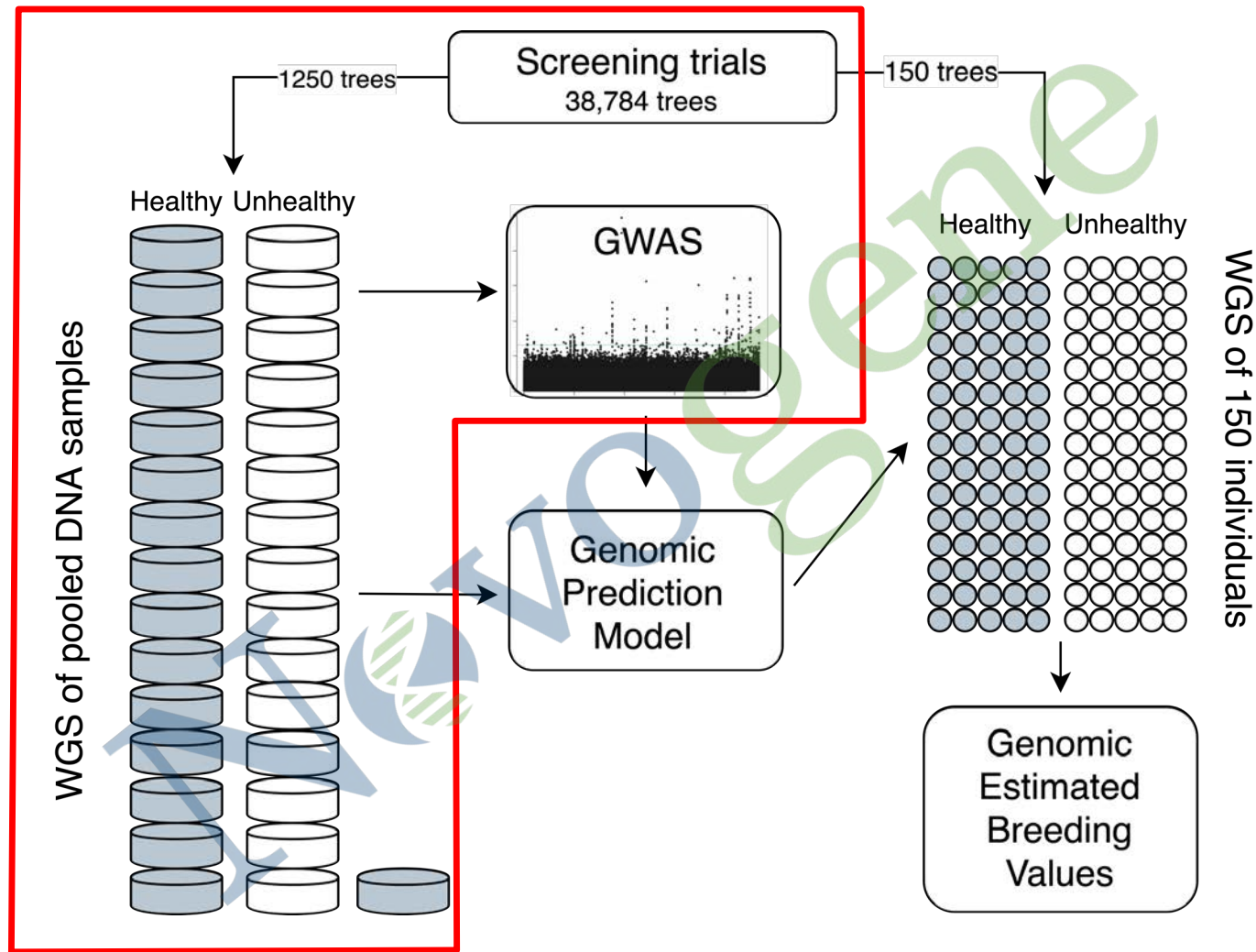
Autumn 2016 results for North Burlingham, Norfolk

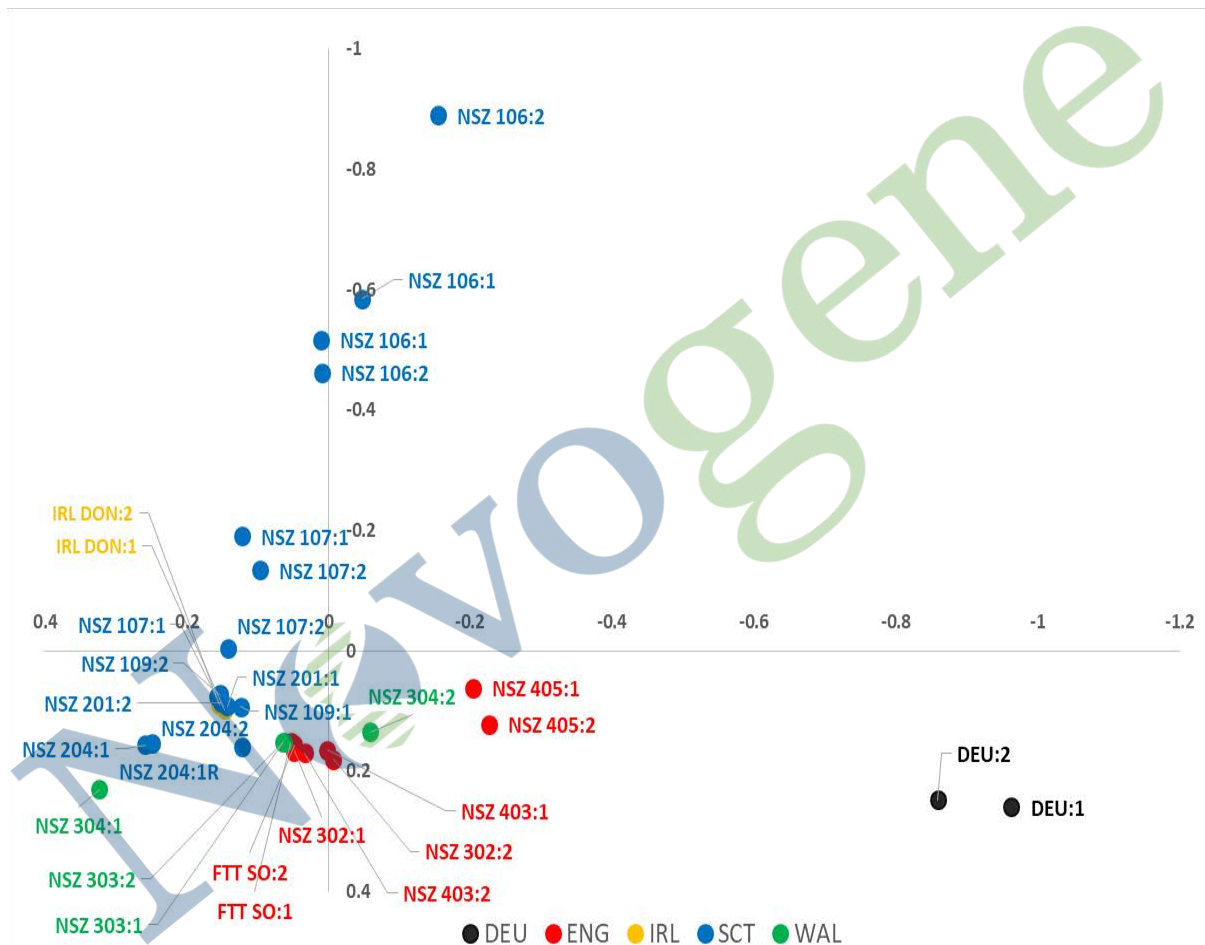
(a) Site 16



LEGEND. Tree Scores: 0 1 2 3 4 5 6 7

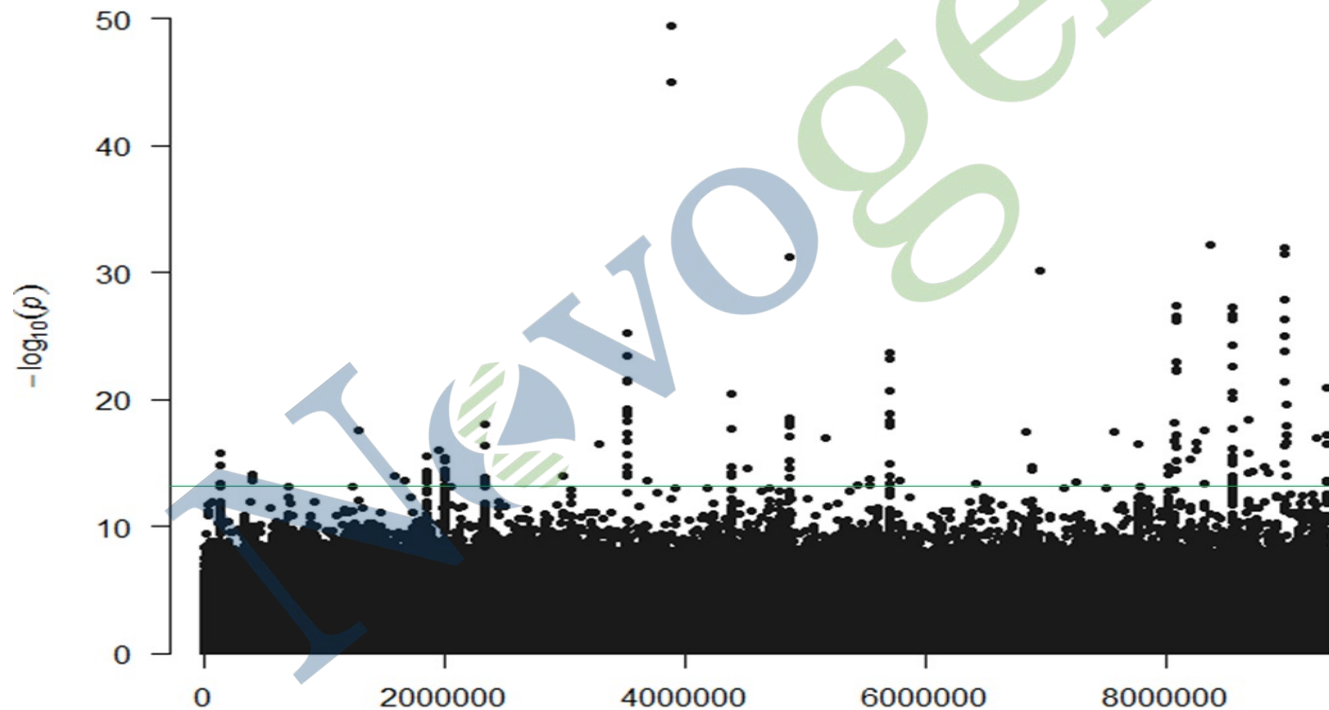
Scientific Reports
7: 16546

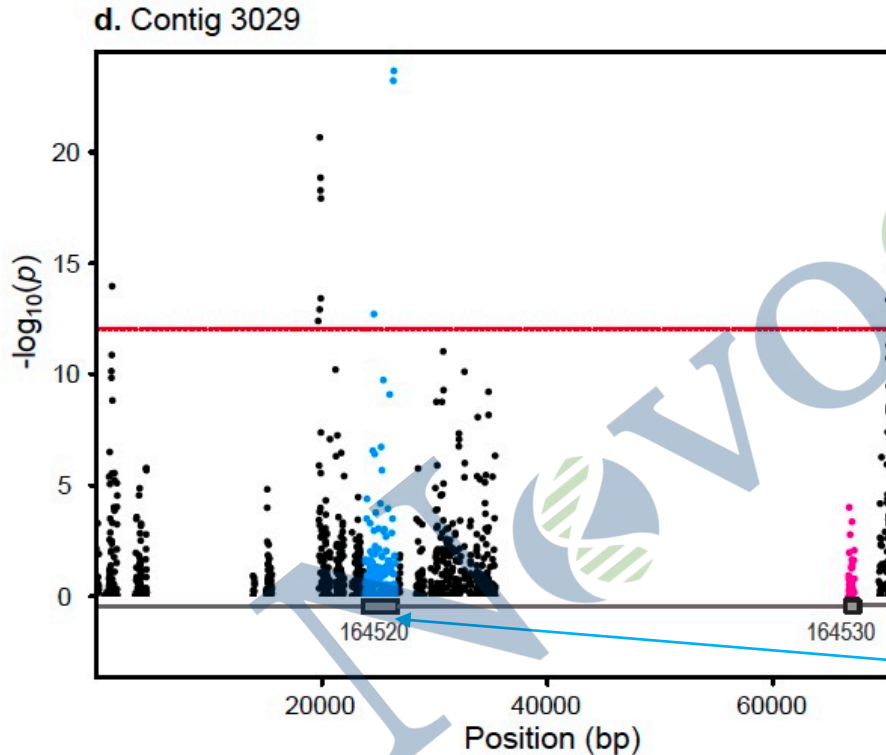




GWAS on pool-seq data

203 SNPs with $-\log_{10}(p) > 13$



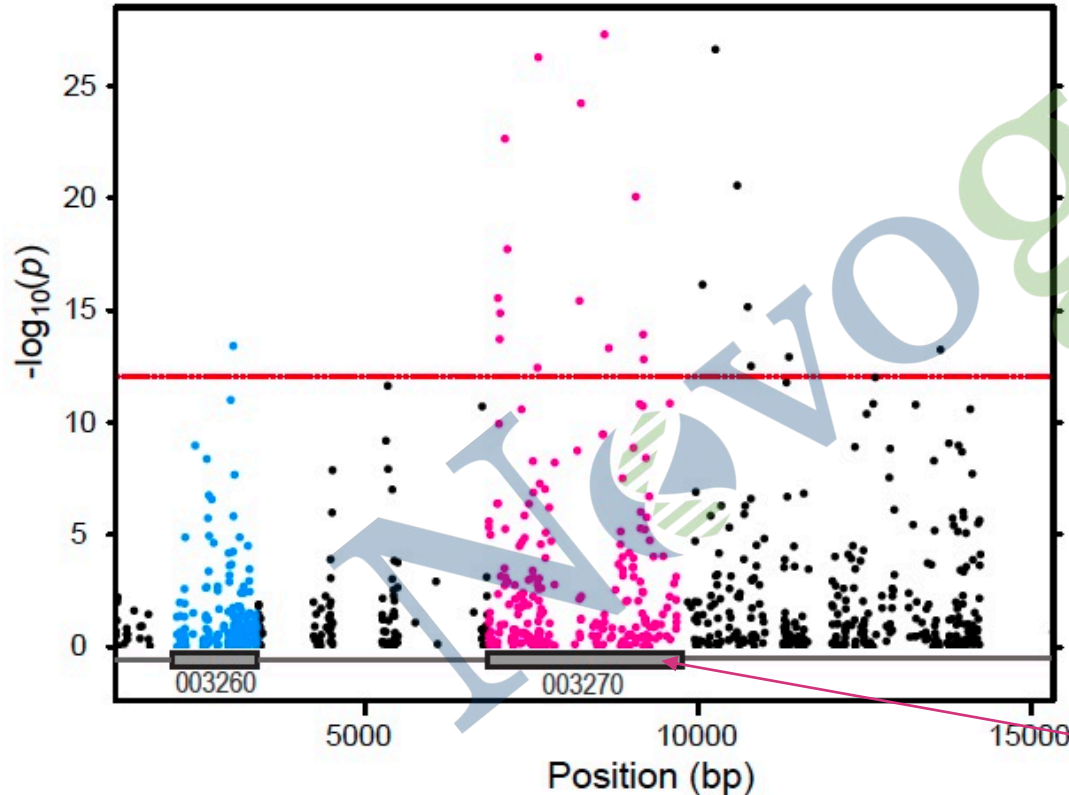


Functional Variants:

1 x missense,
1 x 5' UTR,
2 x downstream

**F-box/kelch-repeat protein
SKIP6** – Plant F-box genes control
many crucial processes including
pathogen resistance

f. Contig 10122



Functional Variants:

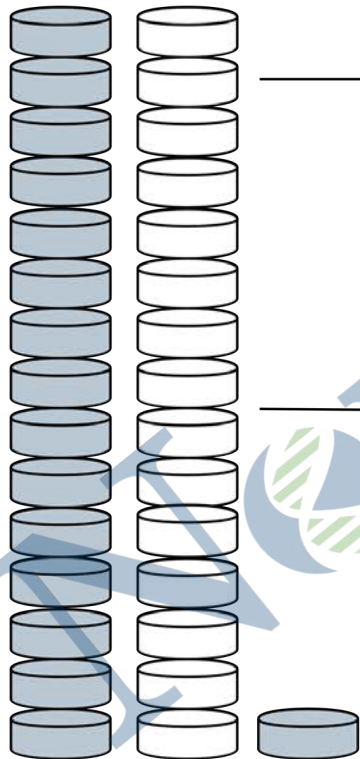
- 1 x missense,
- 1 x intron
- 5 x upstream
- 1 x 5' UTR,
- 1 x 3' UTR
- 1 x downstream

Protein CPR-5-like

CPR5 modulates salicylic acid and the unfolded protein response to manage tradeoffs between plant growth and stress responses (including pathogen attack).

WGS of pooled DNA samples

Healthy Unhealthy



1250 trees

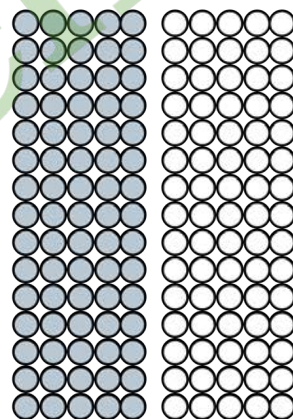
Screening trials
38,784 trees

GWAS

Genomic
Prediction
Model

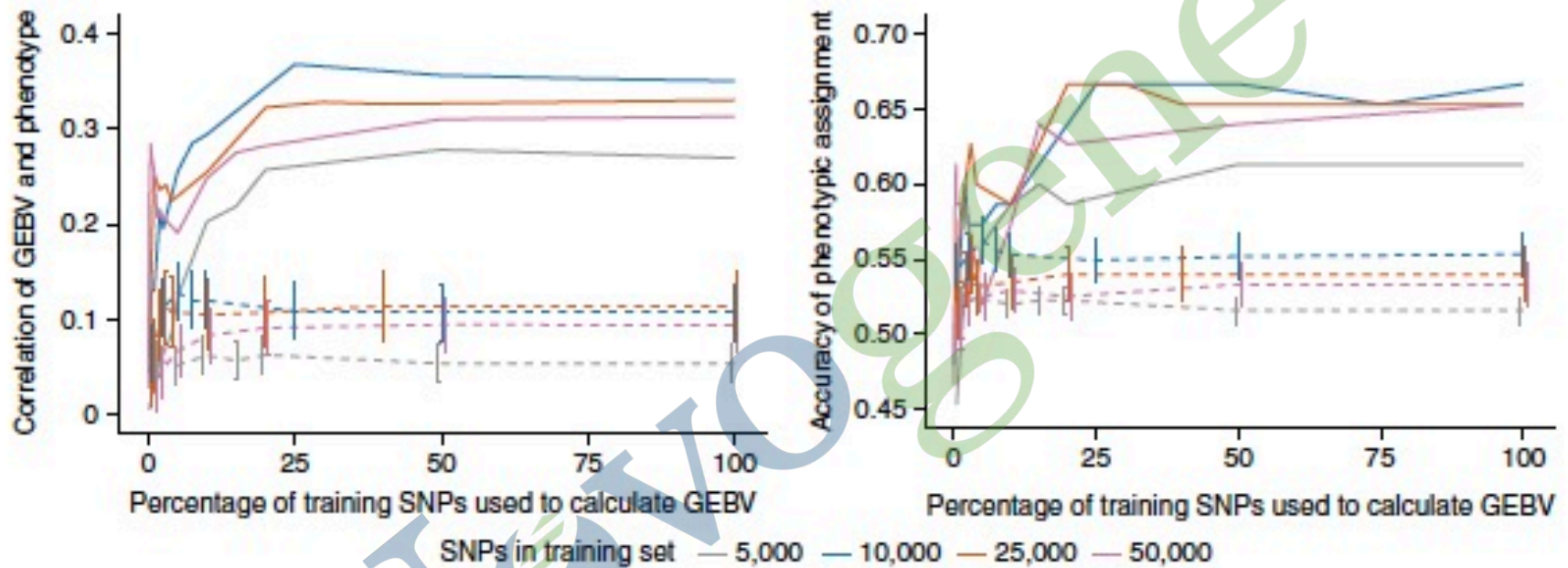
150 trees

Healthy Unhealthy



WGS of 150 individuals

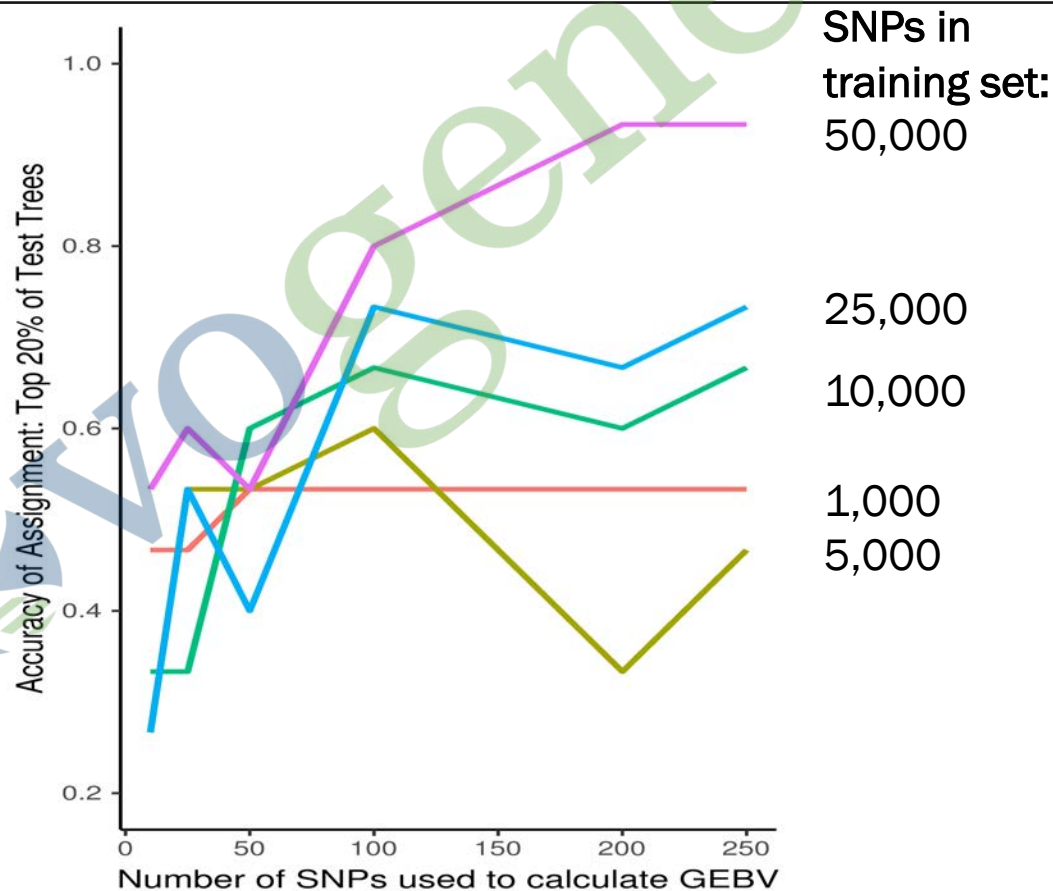
Genomic
Estimated
Breeding
Values



Performance of genomic prediction models for health under ash dieback pressure.

Genomic prediction

Accuracy of
assignment of top
20% of trees by
Genomic
Estimated
Breeding Value
(GEBV) to correct
health status





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**Marden
Park
Wood**

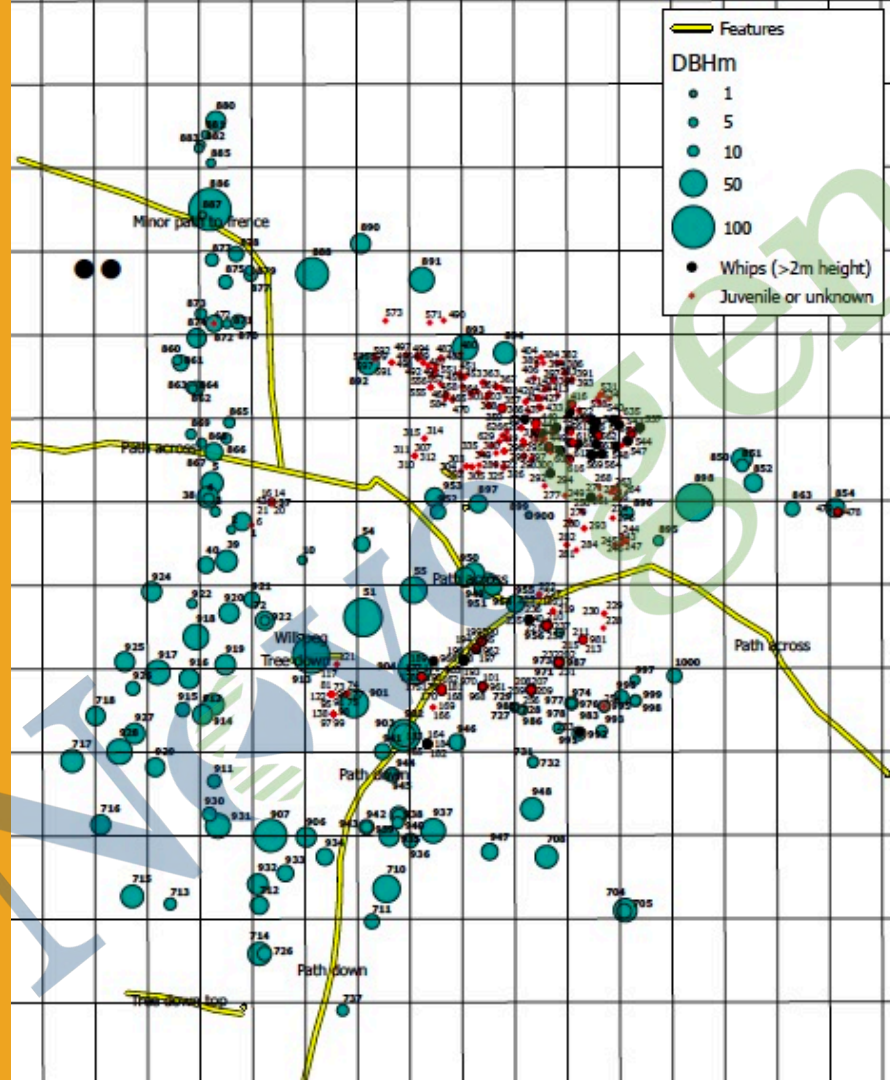


WOODLAND
TRUST

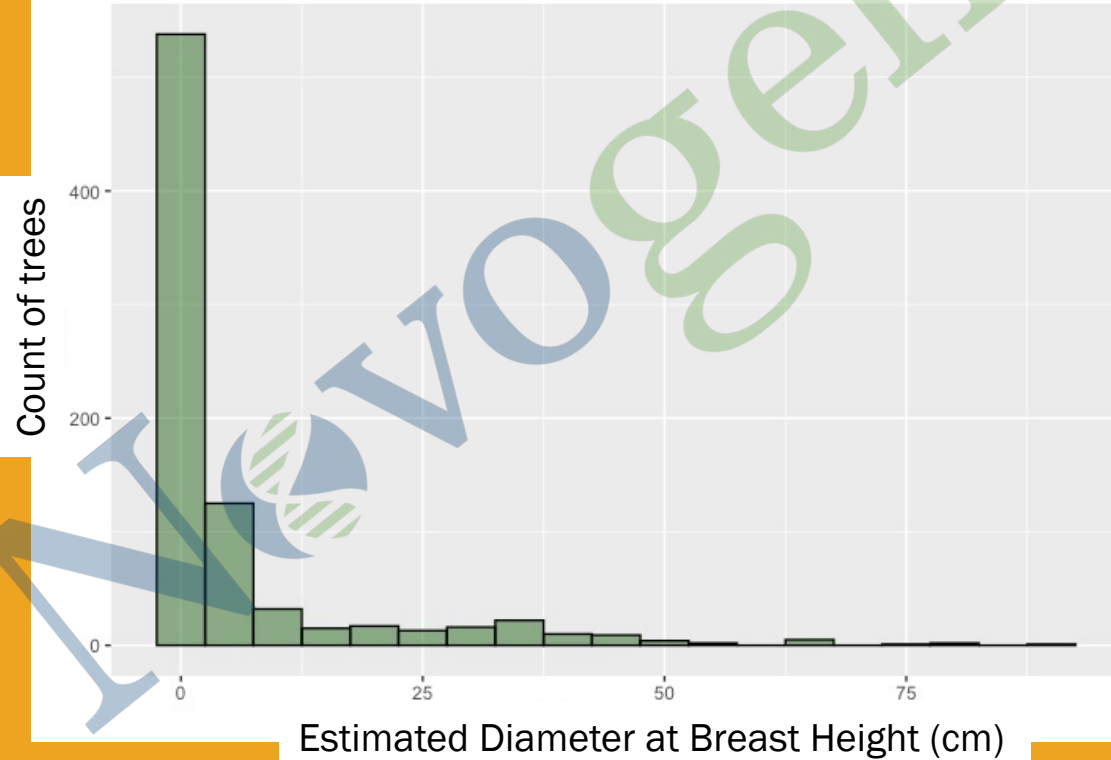
Hypotheses:

- (1) Frequencies of alleles at some loci will consistently co-vary with level of ash dieback damage, so we can predict the ash dieback damage of individual trees
- (2) Many of these loci will be those that were found in our previous study
- (3) Smaller, younger trees will contain a biased subset of the variation present in the adult trees, due to more rapid selection among them by *Hymenoscyphus fraxineus*.

Thus, we hope to detect the action of natural selection in real time in a natural multi-generational population.

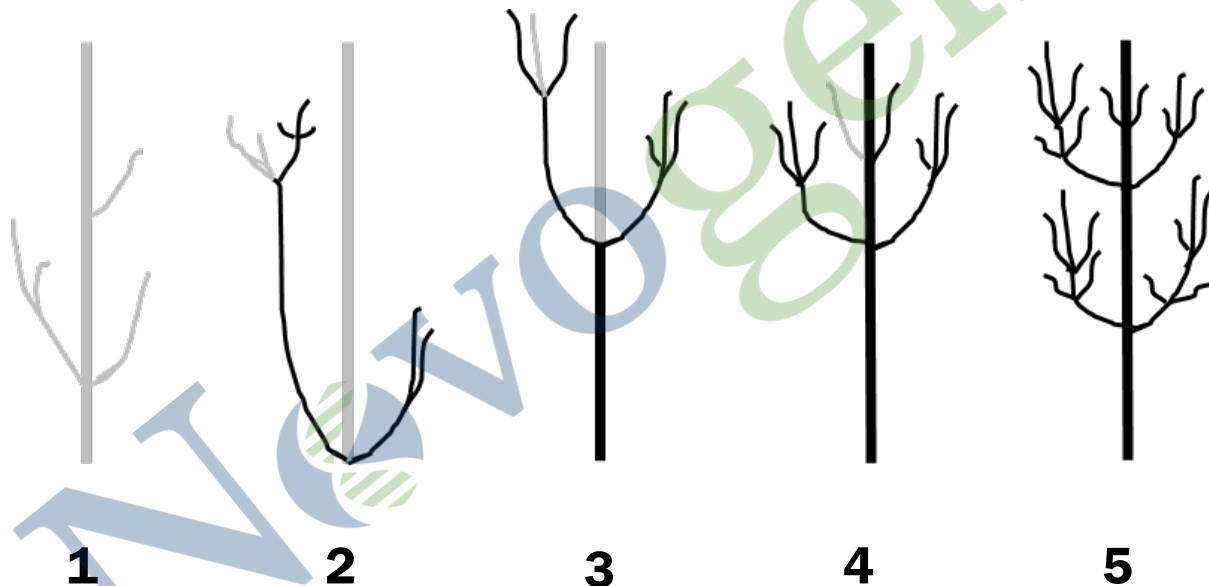


Histogram of measured and estimated diameter (n = 812)

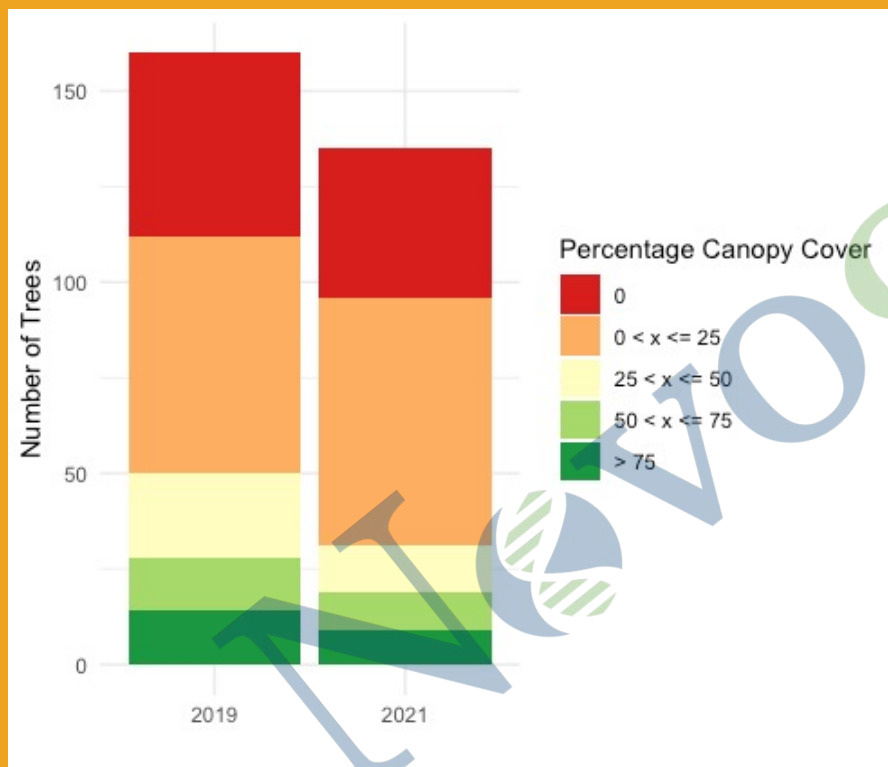




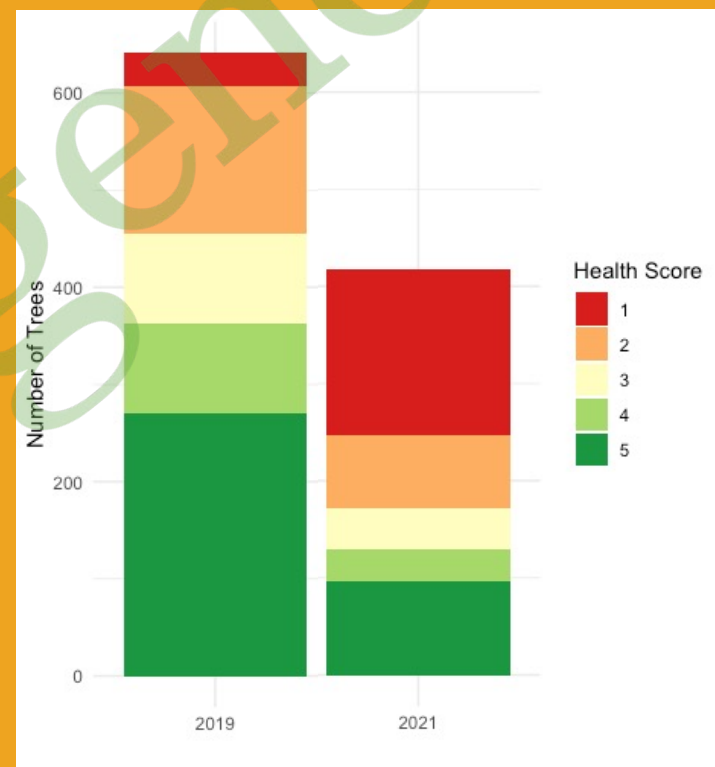








Large trees



Small trees





600 trees sequenced at approx. 10X coverage

Illumina by Novogene

4.5M to 213.8M per sample

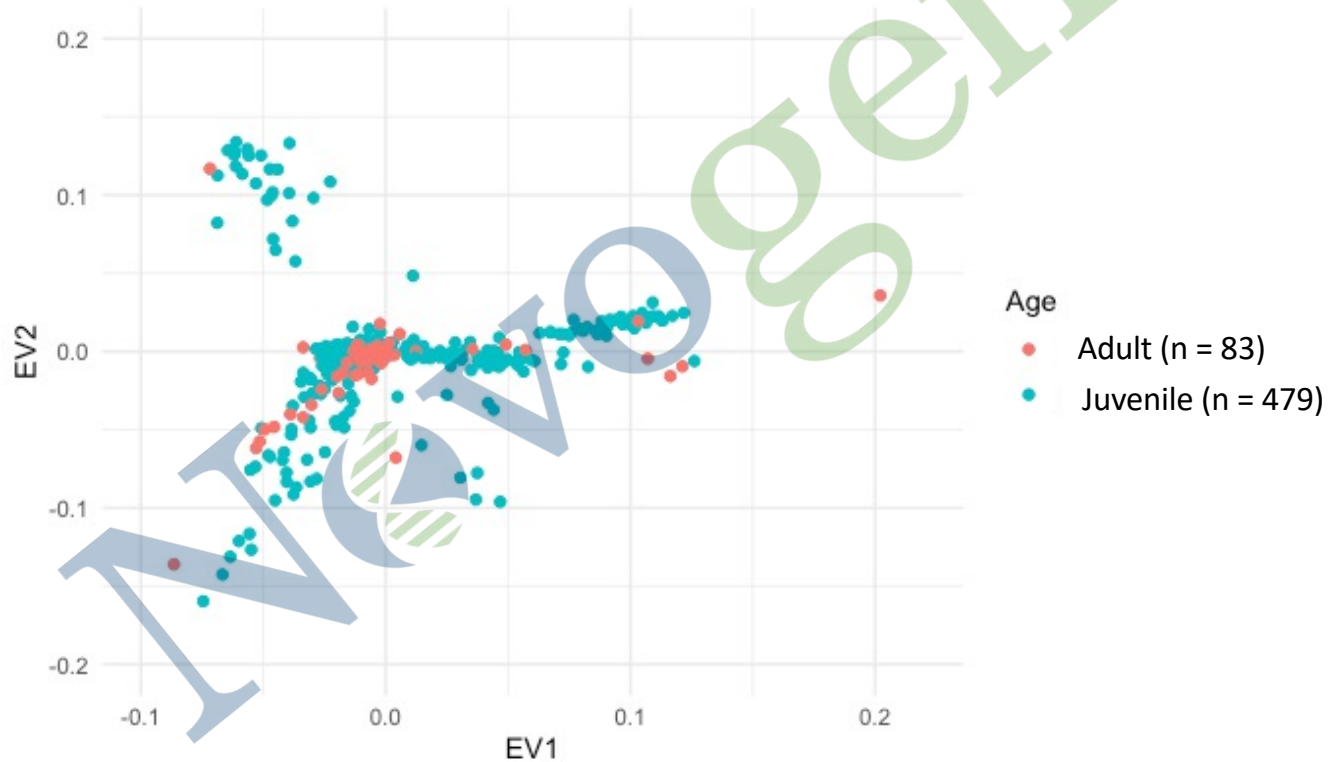
Mean of 71.5M reads per sample

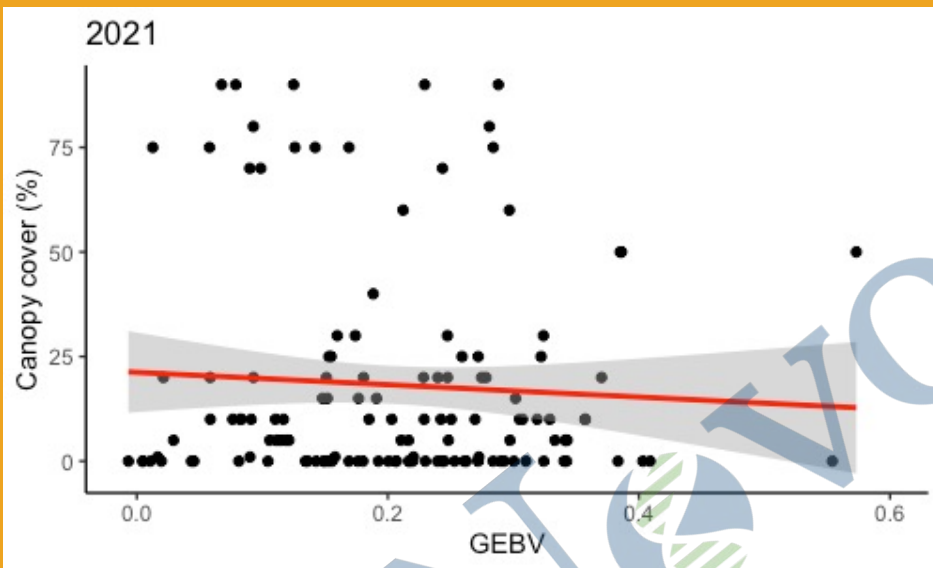
21,336,502 SNPs found

Carey
Metheringham

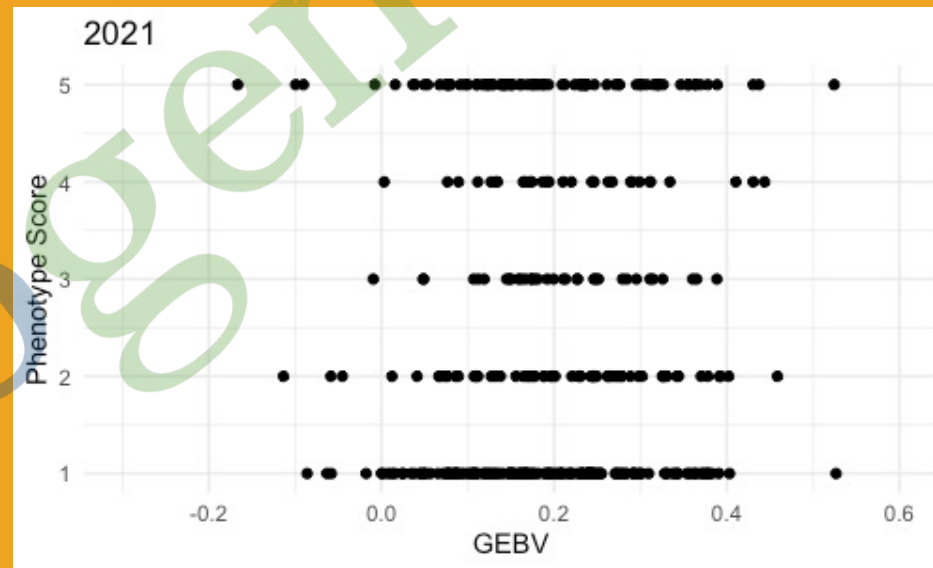


PCA summary of SNP variation



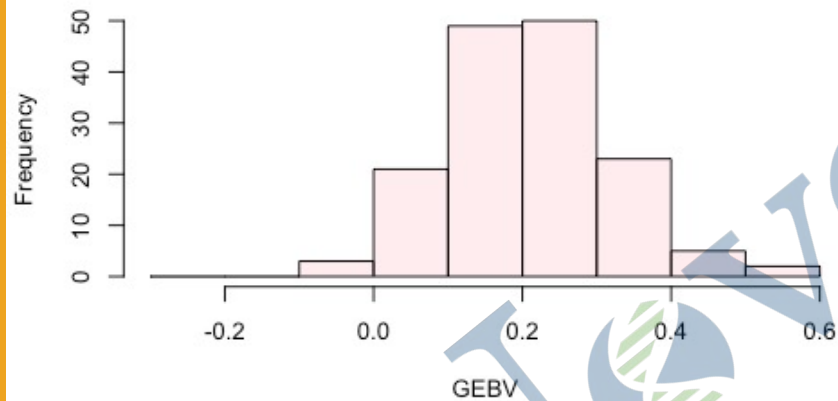


Large trees



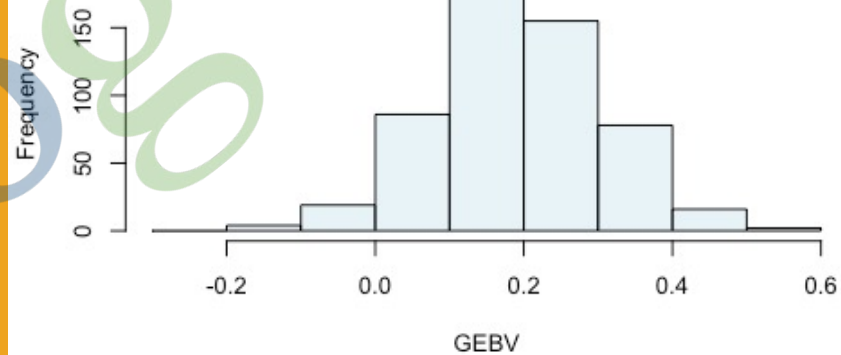
Small trees

GEBV of 153 Adult Trees



Large trees

GEBV of 549 Juvenile Trees



Small trees



Postdocs



Dr Laura Kelly



Dr Endymion Cooper



Dr Tim Coker



Department
for Environment
Food & Rural Affairs

PhD students

Lizzy
Sollars



Jonathan
Stocks



Carey
Metheringham



Jasmin
Zohren



Will Plumb



Collaborators

Richard Nichols (QMUL)
Steve Lee (Forest Research)
Justin Moat (Kew)



Funding:

Royal Botanic Gardens
Kew



Department
for Environment
Food & Rural Affairs

